

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:41 ; Search time 2351.15 Seconds

(without alignments)  
161.385 Million cell updates/sec

Title: US-09-851-670-15

Perfect score: 23  
Sequence: 1 aacgtgtcgcgtctcagagaca 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: gb\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hgtg\_hum:\*  
31: em\_hgtg\_inv:\*  
32: em\_hgtg\_rod:\*  
33: em\_hgtg\_hum:\*  
34: em\_hgtg\_inv:\*  
35: em\_hgtg\_rod:\*  
36: em\_hgtg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	63.5	48	9	S56760 BCL2 {fragm
2	13.4	58.3	55	10	S77019 c-myc...Ig
3	13	56.5	28	6	AX034687 Sequence
4	13	56.5	57	6	AR009400 Sequence
5	13	56.5	58	10	AF557324 Sequence
6	12.8	55.7	24	6	A08385 Mus muscu
7	12.8	55.7	27	6	A08384 Synthetic D
8	12.8	55.7	27	6	AX069493 Sequence
9	12.8	55.7	27	6	AX069494 Sequence
10	12.8	55.7	59	5	U33690 Hypentelium
11	12.6	54.8	51	6	AX159789 Sequence
12	12.6	54.8	60	6	AR118184 Sequence
13	12.6	54.8	60	6	E07618 PCR primer
14	12.4	53.9	35	6	AR079998 Sequence
15	12.4	53.9	43	6	AR085924 Sequence
16	12.4	53.9	43	6	AR093310 Sequence
17	12.4	53.9	43	6	AR121680 Sequence
18	12.4	53.9	44	6	AR043085 Sequence
19	12.4	53.9	49	6	AX082373 Sequence
20	12.4	53.9	18	12	AB069089 Synthetic
21	12.2	53.0	19	6	I88029 Sequence 7
22	12.2	53.0	21	6	AX092795 Sequence
23	12.2	53.0	23	6	A99258 Sequence 34
24	12.2	53.0	24	6	A99252 Sequence 28
25	12.2	53.0	42	6	A36507 Sequence 48
26	12.2	53.0	42	6	AR080140 Sequence
27	12.2	53.0	49	6	AR047941 Sequence
28	12.2	53.0	49	6	AX162776 Sequence
29	12.2	53.0	51	6	AR031474 Sequence
30	12.2	53.0	59	6	AX038002 Sequence
31	12	52.2	26	6	AX008530 Sequence
32	12	52.2	37	6	AX008531 Sequence
33	12	52.2	38	6	AX008532 Sequence
34	12	52.2	41	6	AR050326 Sequence
35	12	52.2	46	6	AR043084 Sequence
36	12	52.2	50	6	AX157364 Sequence
37	12	52.2	51	6	AX157786 Sequence
38	12	52.2	51	6	AX165195 Sequence
39	12	52.2	52	6	AR062114 Sequence
40	12	52.2	60	1	S38798 (Junction J
41	11.8	51.3	21	6	AR020925 Sequence
42	11.8	51.3	21	6	AR020927 Sequence
43	11.8	51.3	21	6	AR020928 Sequence
44	11.8	51.3	21	6	AR051048 Sequence
45	11.8	51.3	21	6	AR051050 Sequence

## ALIGNMENTS

RESULT	1	LOCUS	556760	DEFINITION	BCL2 {fragment 2, translocation breakpoint, variant cluster region}	ACCESSION	556760	VERSION	556760	KEYWORDS	556760.1 GI:299253	SOURCE	human peripheral blood cells.	ORGANISM	Homo sapiens	REFERENCE	Seite,P., Leroux,D., Hillion,J., Montell,M., Berger,R., Mathieu-Manu,D. and Larsen,C.J.	TITLE	Molecular analysis of a variant 18:22 translocation in a case of lymphocytic lymphoma	JOURNAL	Genes Chromosomes Cancer 6 (1), 39-44 (1993)	MEDLINE	93183802	REMARK	Genbank staff at the National Library of Medicine created this
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entry [NCBI g1bbsq 127183] from the original journal article.  
This sequence comes from Fig. 3.  
Map location: t(18;22).

## FEATURES

source  
1..48  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
1..48  
/partial  
/gene="BCL2"  
BASE COUNT 7 a 10 c 22 g 9 t  
ORIGIN

Query Match 63.5%; Score 14.6; DB 9; Length 48;  
Best Local Similarity 81.0%; Pred. No. 1e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23  
11 11 11 11 11 11 11 11  
Db 20 CCGGTGGGTCGTCCGAGACA 40

RESULT 2  
S77019 55 bp DNA ROD 27-JUL-1995  
LOCUS c-myc. : Ig gamma-2b (translocation) [mlce, transgenic, genomic, 3  
DEFINITION genes, 55 nt].  
ACCESSION S77019  
VERSION S77019.1 GI:913974  
KEYWORDS  
SOURCE Mus sp. transgenic.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Martin, M.C., Hsu, B., Stephens, L.C., Brisbay, S. and McDonnell, T.J.  
TITLE The functional basis of c-myc and bcl-2 complementation during  
multistep lymphomagenesis in vivo  
JOURNAL Exp. Cell Res. 217 (2), 240-247 (1995)  
MEDLINE 95212436  
REMARK

Genbank staff at the National Library of Medicine created this  
entry [NCBI g1bbsq 163932] from the original journal article.  
This sequence comes from Fig. 1.  
Map location: t(12;15).

## FEATURES

source  
1..55  
/organism="Mus sp."  
/db\_xref="taxon:10095"  
1..24  
/partial  
/gene="c-myc"  
1..55  
/partial  
/gene="c-myc"  
/gene="c-myc-Ig gamma 2b"  
/note="fusion gene"  
29..55  
/partial  
/gene="Ig gamma-2b"  
BASE COUNT 15 a 15 c 15 g 10 t  
ORIGIN

Query Match 58.3%; Score 13.4; DB 10; Length 55;  
Best Local Similarity 73.9%; Pred. No. 4.2e+04;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 aacgtgctcctcagagaca 23  
11 11 11 11 11 11 11 11  
Db 30 AAGCTCTCAGTCTTAAGAGACA 52

RESULT 3

AX034687 AX034687 28 bp DNA PAT 15-NOV-2000  
LOCUS Sequence 24 from Patent EP1035206.  
DEFINITION  
ACCESSION AX034687  
VERSION AX034687.1 GI:11190661  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequence.

REFERENCE  
AUTHORS Hoshino, T., Ojima, K. and Setoguchi, Y.  
TITLE Astaxanthin synthetase  
JOURNAL Patent: EP 1035206-A 24 13-SEP-2000;  
HOFFMANN LA ROCHE (CH)  
location/Qualifiers

FEATURES  
source  
1..28  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="antisense primer for construction of RPI terminator  
cassette"  
BASE COUNT 6 a 9 c 9 g 4 t  
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 28;  
Best Local Similarity 76.2%; Pred. No. 7.5e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23  
11 11 11 11 11 11 11 11  
Db 7 CGTGGCGAGTCGACCGAGACA 27

RESULT 4  
AR009400 AR009400 57 bp DNA PAT 04-DEC-1998  
LOCUS Sequence 168 from patent US 5756291.  
DEFINITION  
ACCESSION AR009400  
VERSION AR009400.1 GI:3968205  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Griffith, L., Albrecht, G., Latham, J., Leung, L., Vermaas, E. and  
Toole, J.J.  
TITLE Aptamers specific for biomolecules and methods of making  
JOURNAL Patent: US 5756291-A 168 26-MAY-1998;  
MEDLINE  
REMARK location/Qualifiers

FEATURES  
source  
1..57  
/organism="unknown"  
BASE COUNT 10 a 10 c 22 g 9 t 6 others  
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 57;  
Best Local Similarity 76.2%; Pred. No. 6.8e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 cgtgtcggtcctcagagaca 23  
11 11 11 11 11 11 11 11  
Db 9 CCGATGCGGTCTCAGAGACA 29

RESULT 5  
AF357324 AF357324 58 bp RNA ROD 06-JUN-2001  
LOCUS Mus musculus clone MBL1-142 C/D box snRNA, partial sequence.  
DEFINITION  
ACCESSION AF357324  
VERSION AF357324.1 GI:14276919  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 58)  
AUTHORS Huttenhofer,A., Kieffmann,M., Meier-Ewert,S., O'Brien,J.,  
Lehrach,H., Bachelierie,J.-P. and Brosius,J.  
TITLE RNCmics: an experimental approach that identifies 201 candidates  
for novel, small, non-messenger RNAs in mouse  
JOURNAL EMO J. 20 (11), 2943-2953 (2001)  
PUBMED 11387227  
REFERENCE 2 (bases 1 to 58)  
AUTHORS Huttenhofer,A., Kieffmann,M., Meier-Ewert,S., O'Brien,J.,  
Lehrach,H., Bachelierie,J.-P. and Brosius,J.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2001) Institute of Experimental Pathology /  
Molecular Neurobiology, ZMBE, University of Muenster,  
Von-Esmarch-Str. 56, Muenster D-48149, Germany

FEATURES  
source Location/Qualifiers  
1..58  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="MBII-142"  
misc\_RNA  
1..38  
/note="missing at least 5-10 bases"  
/product="C/D box snRNA: small non-messenger RNA  
(snmRNA)"

BASE COUNT 14 a 13 c 20 g 11 t  
ORIGIN

Query Match 56.5%; Score 13; DB 10; Length 58;  
Best Local Similarity 76.2%; Pred. No. 6.7e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctcagagac 22  
||||| || ||| |||||  
DB 10 ACGTGTCGGCCACTGAGAC 30

RESULT 6  
A08385/c A08385 24 bp DNA PAT 26-AUG-1993  
LOCUS A08385  
DEFINITION Synthetic DNA sequence for primate prolinsulin, Reverse complement.  
ACCESSION A08385  
VERSION A08385.1 GI:411636  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Doerschug,M.  
TITLE Insulin derivatives, their use and a pharmaceutical composition  
JOURNAL containing same  
PATENT: EP 0368187-A 8 16-MAY-1990;  
HOECHST AKTIENGESellschaft  
FEATURES  
source Location/Qualifiers  
1..24  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 5 a 5 c 9 g 5 t  
ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctca 17  
||||| ||||| |||||  
DB 17 ACCTGTGCGGTCTCA 2

RESULT 7  
A08384 A08384

LOCUS A08384 27 bp DNA PAT 26-AUG-1993  
DEFINITION Synthetic DNA sequence for primate prolinsulin.  
ACCESSION A08384  
VERSION A08384.1 GI:413447  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Doerschug,M.  
TITLE Insulin derivatives, their use and a pharmaceutical composition  
JOURNAL containing same  
PATENT: EP 0368187-A 7 16-MAY-1990;  
HOECHST AKTIENGESellschaft  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 6 a 10 c 5 g 6 t  
ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 27;  
Best Local Similarity 87.5%; Pred. No. 9.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acgtgtgcggtcctca 17  
||||| ||||| |||||  
DB 8 ACCTGTGCGGTCTCA 23

RESULT 8  
AX069493/c AX069493 27 bp DNA PAT 25-JAN-2001  
LOCUS AX069493  
DEFINITION Sequence 157 from Patent WO0102600.  
ACCESSION AX069493  
VERSION AX069493.1 GI:12579278  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Yuan,C.S.  
TITLE Detection of analytes using attenuated enzymes  
JOURNAL Patent: WO 0102600-A 157 11-JAN-2001;  
GENERAL ATOMICS (US)  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotides for producing SAM hydrolase  
mutants"

BASE COUNT 6 a 8 c 9 g 4 t  
ORIGIN

Query Match 55.7%; Score 12.8; DB 6; Length 27;  
Best Local Similarity 87.5%; Pred. No. 9.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gtgcggtcctcagaga 21  
||||| ||||| |||||  
DB 20 GTGCTGCTCTCAGAGA 5

RESULT 9  
AX069494 AX069494 27 bp DNA PAT 25-JAN-2001  
LOCUS AX069494  
DEFINITION Sequence 158 from Patent WO0102600.  
ACCESSION AX069494  
VERSION AX069494.1 GI:12579279  
KEYWORDS  
SOURCE synthetic construct.



## ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 60)  
 AUTHORS Honjo, T. and Shimizu, A.  
 TITLE Interleukin 2 receptor and a method for production thereof  
 JOURNAL Patent: US 4816565-A 4 28-MAR-1989;  
 Tasaku Honjo;  
 Toyonaka, JP;

## FEATURES

source

Location/Qualifiers  
 1..60  
 /organism="unknown"

## BASE COUNT

10 a 16 c 18 g 16 t

## ORIGIN

Query Match 54.8%; Score 12.6; DB 6; Length 60;  
 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 aacgtgtcggtcctcagac 19  
 ||||| ||||| |||

DB 35 AACGTGACGAGTCCACACA 17

## RESULT 14

LOCUS E07618

35 bp DNA

PAT 29-SEP-1997

DEFINITION PCR primer.

ACCESSION E07618

VERSION E07618.1 GI:2175753

KEYWORDS JP 1994153967-A/3.

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 35)

TANIDA, M., YAGI, S., HASEGAWA, A., RA, T. and OKUMURA, Y.

PRODUCTION OF ALPHA-CHAIN OF SOLUBLE IGE BINDING RECEPTOR BY YEAST

PATENT: JP 1994153967-A 3 03-JUN-1994;

TOMEN CORP, RA TOMOYASU

## COMMENT

OS

None

OC Artificial sequences.

PN

JP 1994153967-A/3

PD

03-JUN-1994

PF

18-NOV-1992 JP 1992308896

PI

TANIDA MCHIMASHI, YAGI SHINTARO, HASEGAWA AKIRA, RA TOMOYASU,

PI

OKUMURA YASUSHI

PC

C12N15/62, C07K3/02, C07K15/04, C12N1/19, C12N15/13, C12N15/81, PC

C12P21/02,

PC

(C12N1/19, C12R1:865), (C12P21/02, C12R1:865);

CC

strandedness: Single;

CC

topology: Linear;

FH

key

## FEATURES

source

1..35

Location/Qualifiers

1..35

/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT

12 a 11 c 6 g 6 t

ORIGIN

Query Match 53.9%; Score 12.4; DB 6; Length 35;  
 Best Local Similarity 72.7%; Pred. No. 1.5e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY

1 aacgtgtcggtcctcagac 22

||| | | | | | | | |

DB

24 ACGCTTTCGCTCCTCAGCGTCA 3

Search completed: March 9, 2002, 00:48:43

Job time: 11124 sec

## RESULT 15

AR079998/c

AR079998

43 bp DNA

PAT 31-AUG-2000

LOCUS

Sequence 81 from patent US 5968524.

ACCESSION

AR079998

VERSION

AR079998.1 GI:10006733

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 43)

AUTHORS

Watson, J.D. and Tan, P.L.J.

TITLE

Methods and compounds for the treatment of immunologically-mediated

psoriasis

JOURNAL

Patent: US 5968524-A 81 19-OCT-1999;

FEATURES

Location/Qualifiers

1..43

/organism="unknown"

BASE COUNT

13 a 7 c 18 g 5 t

ORIGIN

Query Match 53.9%; Score 12.4; DB 6; Length 43;  
 Best Local Similarity 72.7%; Pred. No. 1.4e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY

2 aacgtgtcggtcctcagac 23

||| | | | | | | | |

DB

24 ACGCTTTCGCTCCTCAGCGTCA 3

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